# Genomic selection in small holder systems: challenges and opportunities

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# Introduction

- Single nucleotide polymorphism (SNP) is a DNA sequence variation occurring when a single nucleotide in the genome differs between paired chromosomes in an individual.
- Using the association between SNP and QTL for economic traits, genomic breeding values (GEBV) can be computed for animals
- Selection using GEBVs has been implemented for various livestock species and is termed genomic selection

# Benefits of genomic selection

- Benefits of genomic selections have well been demonstrated

  in developed countries

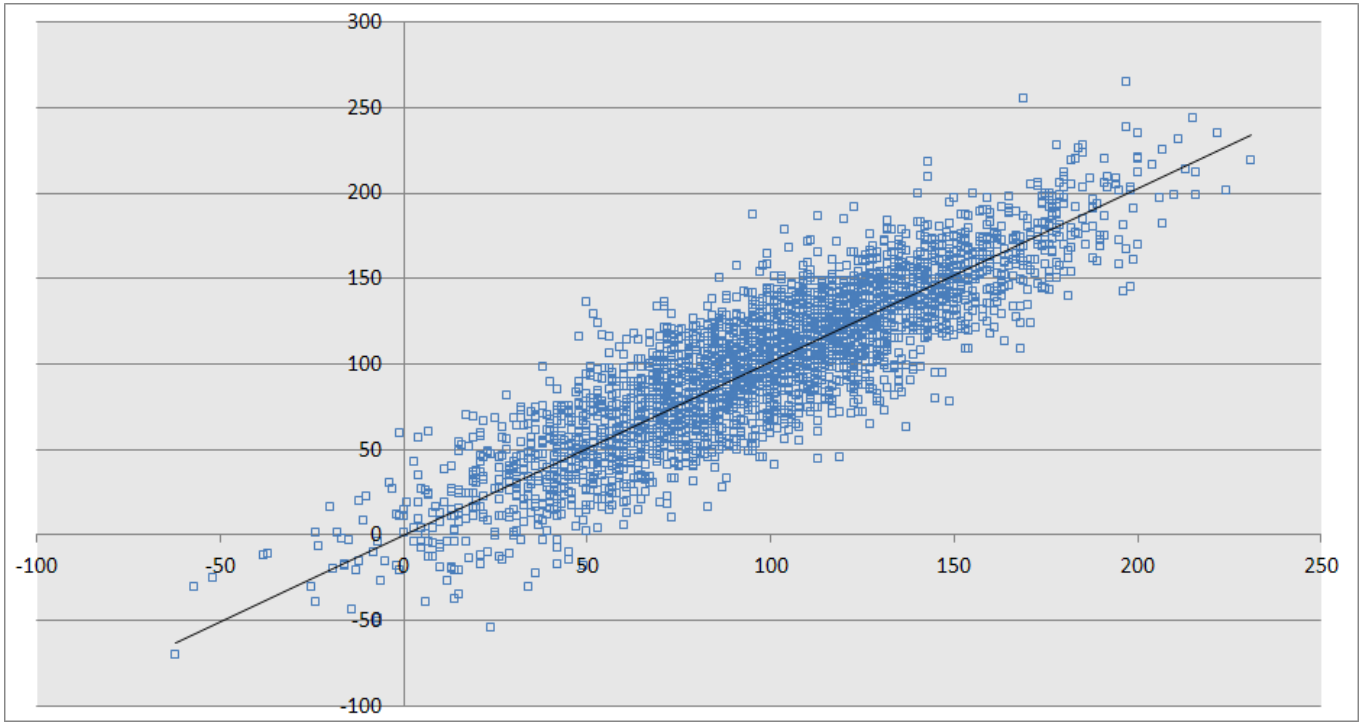
  - Reduced generation interval
  - Accuracies of above 70% have been reported for young genomic proven bulls
  - Higher rates of genetic gains

# UK data that demonstrated that genomics work

- Comparing 3001 bulls
  - April 2012 Young bull genomic indexes
  - December 2013 indexes for the same bulls, but now with daughter performance information

# Genomic → Dtr proven (Apr-12 to Dec-13)

- Correlation = 0.88
- Average April 2012 = £100  PLI  (rlb. 69%)
- Average Dec 2013 = £101 PLI  (rlb. 81%) (+12% rlb increase)



# Characteristics of genomic system in developed countries

- Genomic systems in developed countries are characterised
- With large reference populations
- Collaboration among countries
- Well defined phenotypes
- But mostly within pure breeds

# Characteristics of genomic data in small holder systems

- Challenges:
  - Small data sets
  - Difficult to define good reference and validation populations
  - Little data on pure breeds
  - Mostly on cross-bred animals

# Characteristics of genomic data in small holder systems

- Opportunities:
  - Genotypes on cross-bred animals
  - Explore novel methods adapted to the data structure
  - Collaboration – sharing data and methodologies applied

# Opportunities offered by genomics in small holder systems

- In small holder systems data and pedigree recording posses a challenge.
- Quick wins from genotypic data includes
  - Reduces the need for accurate pedigree recording as genomic relationship can easily be computed
  - Parentage discovery using SNP data
  - Usage to determine the breed composition of cross-bred animals in the absence of pedigree.
    - Gives the opportunity to match different genotypes to different management systems
  - Future use in traceability of animal products

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# Demonstrate some of the challenges & opportunities in small holder genomic data

- Examine genomic prediction using the DGEA small holder data
- GBLUP with **G** matrix was formed
    - Using SNP alleles frequencies from all cross-breds for scaling
- Attempt was made to determine accuracy of genomic prediction from subsets of the population with different breed composition

# The DGEA data

- Data consisted of 1038 cows genotyped with the 777K Illumina High density chip
- Cows from 5 random sites in dairy production areas in Kenya
- Test day milk records were available
- Yield deviations for milk yield were generated using a repeatability model

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# Classification of cows by breed composition.

| Dairy% | Breedtype | | Dairy%by-Breedtype |
|---|---|---|---|
| 1 (0-20%) | Zebu | 6 | 1 |
| 2 (0.33-35%) | Mixed + Zebu | 6 | 2 |
| 3 (36-60%) | Ayr/Gue/Jer | 1 | 3 |
| 3 | Fri | 2 | 4 |
| 3 | Mixed + Zebu | 6 | 5 |
| 4 (61-87.5%) | Ayr | 1 | 6 |
| 4 | Fri | 2 | 7 |
| 4 | Ayr/Fri | 3 | 8 |
| 4 | Gue/Fri | 4 | 9 |
| 4 | Ayr/Gue/Fri | 5 | 10 |
| 4 | Mixed + Zebu | 6 | 11 |
| 5(>87.5%) | Ayr | 1 | 12 |
| 5 | Fri | 2 | 13 |
| 5 | Ayr/Fri | 3 | 14 |
| 5 | Gue/Fri | 4 | 15 |
| 5 | Gue/Fri/Ayr | 5 | 16 |

# Average relationship from G matrix using breed type

| | | | | | | |
|---|---|---|---|---|---|---|
| **1** | **0.027** | | | | | |
| **2** | **0.016** | **0.018** | | | | |
| **3** | **0.026** | **0.022** | **0.038** | | | |
| **4** | **0.022** | **0.021** | **0.032** | **0.035** | | |
| **5** | **0.030** | **0.024** | **0.042** | **0.041** | **0.051** | |
| **6** | **0.024** | **0.016** | **0.003** | **0.003** | **0.001** | **0.118** |

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# Maximum relationship from G matrix

| | | | | | | |
|---|---|---|---|---|---|---|
| 1 | 0.590 | | | | | |
| 2 | 0.591 | 0.564 | | | | |
| 3 | 0.608 | 0.586 | 0.602 | | | |
| 4 | 0.413 | 0.539 | 0.520 | 0.565 | | |
| 5 | 0.242 | 0.308 | 0.564 | 0.561 | 0.484 | |
| 6 | 0.516 | 0.546 | 0.535 | 0.506 | 0.269 | 0.681 |

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# Accuracy of prediction for Zebu and Zebu+mixed crosses

| | | | | | |
|---|---|---|---|---|---|
| **mean & std** | **176** | **-0.6149** | **-0.5818** | **1.0750** | **0.2728** |
| **reg & corr** | **176** | **1.2563** | **0.3188** | | |
| **mean & sd of diff** | **2** | **176** | **0.0332** | **1.0213** | |

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# Accuracy of prediction for cows with 61-87.5% Dairy

| | | | | | |
|---|---|---|---|---|---|
| **mean & std** | **448** | **0.0000** | **0.0276** | **1.3368** | **0.2386** |
| **reg & corr** | | **1.9413** | **0.3465** | | |
| **mean & sd of diff** | | **0.0276** | **1.2740** | | |

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# Accuracy of prediction for cows with greater than 87.5% Dairy

| | | | | | |
|---|---|---|---|---|---|
| **mean & std** | **297** | **0.3961** | **0.2868** | **1.5969** | **0.2200** |
| **reg & corr** | | **2.9743** | **0.4098** | | |
| **mean & sd of diff** | | **-0.1093** | **1.5201** | | |

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# Implications and opportunities of such accuracies

- Given data structure and size, accuracies of genomic prediction obtained are encouraging
- Can be used to identify extreme animals on performance
- Can be used to select team of young bulls to use as sires
- Reduction in generation interval with use of young bulls will result in increase rate of productivity

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# Implications and opportunities of such accuracies

- Need for more data.
- The common saying is that in the “era of genomics, the phenotype is king”
- Looking at smart and innovative digital ways to collect data in the proposed Africa dairy genetics gain project

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# Implications and opportunities of such accuracies

- Need for collaboration across countries. This has been key for application of genomics
- Only third of the 20,000 bulls in the reference pop for the German genomic system are home proven.
- In the UK, less than one third of 22,000 bulls in the reference pop are domestic bulls
- Across regional genomics might be necessary for application of genomics for small holder farmers
    - Possibly most exotics sires used in crossing breeding are similar across regions or countries
    - Policies that promote easy flow of data across country boundaries while maintaining data security and ownership will be needed

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# Implications and Opportunities of such accuracies

- Need to collaborate with developed countries where some of the sires of these cows could have been genotyped
    - Parentage discovery & determine breed composition
    - Genotype by environmental interaction if enough data
- Link small holder data to medium to large farms enabling applications of methods such as one step
- Genotypes on cross-breds offer a unique opportunity and approach to examining across breed genomics

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# Conclusions

- Genomics offers quick wins in small holder systems through use of genomic relationship matrix and parentage discovery reducing need for accurate pedigree.
- Given data structure for smaller , well adapted methodologies will be needed for genomic selection but initial results are encouraging
- Collaboration on across country or regional basis will be needed to ensure adequate data and  best sires can be used across regions
- Genotyping of cross bred animals offers possibilities for further optimize cross breeding systems
- In general, genotypic data offers opportunities to model underling genetics for production and resilience and therefore provide ways to modify them even in wild life populations

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